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**cDNA Sequence of human IBR**

**Two alternativ 5' ends:**

1 TTGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAA
2 AAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAA

**Common Sequence:**

AGGGGAGTCTACACCCTGTGGAGCTCAAGATGGTCCTGAGTGGGGCGCTGTGCTTCCGAA 60
TGAAGGACTCGGCATTGAAGGTGCTTTATCTGCATAATAACCAGCTTCTAGCTGGAGGGC 120
TGCATGCAGGGAAGGTCATTAAAGGTGAAGAGATCAGCGTGGTCCCCAATCGGTGGCTGG 180
ATGCCAGCCTGTCCCCCGTCATCCTGGGTGTCCAGGGTGGAAGCCAGTGCCTGTCATGTG 240
GGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGGAGCTCTATCTTG 300
GTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACCTCCAGCT 360
TCGAGTCGGCTGCCTACCCGGGCTGGTTCCTGTGCACGGTGCCTGAAGCCGATCAGCCTG 420
TCAGACTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCCATCACAGACTTCTACT 480
TCCAGCAGTGTGACTAGGGCAACGTGCCCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGG 540
GTGAGGGGTGAGTGGAGGAGACCCATGGCGGACAATCACTCTTTCTGCTCTCAGGACCCC 600
CAGGTCTGACTTAGTGGGCACCTGACCACTTTGTCTTCTGGTTCCCAGTTTGCATAAATT 660
CTGAGATTTGGAGCTCAGTCCAGGGTCCTCCCCCACTGGATGGTGCTACTGCTGTGGAAC 720
CTTGTAAAAACCATGTGGGGTAAACTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGG 780
GTGGGGGAGTGCTGGGAATCATTCCTGCTTAATGGTAACTGACAAGTGTTACCCTGAGCC 840
CCGCAGGCCAACCCATCCCCAGTTGAGCCTTATAGGGTCAGTAGCTCTCCACATGAAGTC 900
CTCTCACTCACCACTGTGCAGGAGAGGGAGGTGGTCATAGAGTCAGGGATCTATGGCCCT 960
TGGCCCAGCCCCACCCCCTTCCCTTTATCCTGCCACTGTCATATGCTACCTTTCCTATCT 1020
CTTCCCTCATCATCTTGTTGTGGGCATGAGGAGGTGGTGATGTCAGAAGAAATGGTTCGA 1080
GCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTTAAAAACCCAAGATACAA 1140
TCAAAATCCCAGATGCTGGTCTCTATTCCCATGAAAAAGTGCTCATGACATATTGAGAAG 1200
ACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTAAAAGATACCTATTTATAT 1260
ATTTCTTTATAGAAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTCAGGGTGGT 1320
GGCAGTATAGGTGATTTTTCTTTTAATTCTGTTAATTTATCTGTATTTCCTAATTTTTCT 1380
ACAATGAAGATGAATTCCTTGTATAAAAATAAGAAAAGAAATTAATCTTGAGGTAAGCAG 1440

Fig. 1

AGCAGACATCATCTCTGATTGTCCTCAGCCTGCAATTCCCCAGAGTAAATTCAAATTGAA 1500
TCGAGCTCTGCTGCTCTGGTTGGTTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCC 1560
ACTGAGGAGGAGGCTGTGCTGAGTTTGTGTGGCTGGAATCTCTGGGTAAGGAACTTAAAG 1620
AACAAAAATCATCTGGTAATTCTTTCCTAGAAGGATCACAGCCCCTGGGATTCCAAGGCA 1680
TTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGAATTGTGTCCCCCTCAAATTCAC 1740
ATCCTTCTTGGAATCTCAGTCTGTGAGTTTATTTGGAGATAAGGTCTCTGCAGATGTAGT 1800
TAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATATGACTGGTTTCCT 1860
TGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTAAAGATGA 1920
AGGCAGAGATCGGAGTTTTGCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACCAT 1980
CAGAAGCTTGGAAGAGGCAAAGAAGAATTCTTCCCTAGAGGCTTTAGAGGGATAACGGCT 2040
CTGCTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAATAAATTTCGGC 2100
TGTTTTAAGCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAAACTAATACAGCTGCTA 2160
AAATGATCCCTGTCTCCTCGTGTTTACATTCTGTGTGTGTCCCCTCCCACAATGTACCAA 2220
AGTTGTCTTTGTGACCCAATAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTA 2280
GGTTATAAAAGACACTGCAGCTTCTACTTGAGCCCTCTCTCTCTGCCACCCACCGCCCCC 2340
AATCTATCTTGGCTCACTCGCTCTGGGGGAAGCTAGCTGCCATGCTATGAGCAGGCCTAT 2400
AAAGAGACTTACGTGGTAAAAAATGAAGTCTCCTGCCCACAGCCACATTAGTGAACCTAG 2460
AAGCAGAGACTCTGTGAGATAATCGATGTTTGTTGTTTTAAGTTGCTCAGTTTTGGTCTA 2520
ACTTGTTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG($A_n$) 2562

Fig. 1 (Continued)

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**cDNA Sequence of murine IBR**

GGCACGAGGGGAGCCTGCTTTCTACTTAGGTCTCAAATTTTCCAGCCTTGTCTTTGCCTA 60
AAATTTCCTGCTGTTTATTTCAAAATAGGGTCTACATACTGTGGAGCTCATGATGGTTCT 120
GAGTGGGGCACTATGCTTCCGAATGAAGGATTCAGCCTTGAAGGTACTGTATCTGCACAA 180
TAACCAGCTGCTGGCTGGAGGACTGCACGCAGAGAAGGTCATTAAAGGTGAGGAGATCAG 240
TGTTGTCCCAAATCGGGCACTGGATGCCAGTCTGTCCCCTGTCATCCTGGGCGTTCAAGG 300
AGGAAGCCAGTGCCTATCTTGTGGGACAGAGAAAGGGCCAATTCTGAAACTTGAGCCAGT 360
GAACATCATGGAGCTCTACCTCGGGGCCAAGGAATCAAAGAGCTTCACCTTCTACCGGCG 420
GGATATGGGTCTTACCTCCAGCTTCGAATCCGCTGCCTACCCAGGCTGGTTCCTCTGCAC 480
CTCACCGGAAGCTGACCAGCCTGTCAGGCTCACTCAGATCCCTGAGGACCCCGCCTGGGA 540
TGCTCCCATCACAGACTTCTACTTTCAGCAGTGTGACTAGGGCTGCGTGGTCCCCAAAAC 600
TCCATAAGCAGAGGCAGAGTAGGCAGTGGCGGCTCCTGATAGAGGATAGAGAGACAGAGG 660
AGCTCCACAGTAGGTGGCTTACTCCTCTCCTTCCCTACTGGACTCCCGCTTCTGACCTAA 720
GGCACACAGACACTCTCTTCTCCTGCATCCCAGTGCTGGTAAATCTTCTGGTATTTGGAG 780
CTCAATGTGTAGATTCTTTCAGATTGGATGGTACTACCTCTGGTGTGGAACCCAATAGAA 840
ACCACGTAGGACCAACAAAGAGCAACATAAAAGATTCTTGGGTGAAGAAGAGGTGGGAAC 900
TGTTCATACATAGTAAGATCTGACACAGTACCTCAGAAGTCCTGCCATTCCTTATGTTCT 960
GGAGAAAGTGGAGGGGGGGTCACCAAGACTTTCTCTGGCTGGCTGGGCCCTTTCCCTCAA 1020
CCTTTCTGACATCTGCAGCCTCTCTCATTCTTGCCTTCATTCTCTGGCCCTGAACCGAGA 1080
GGGTGATATCAGGATAGCTGACAGAAGATGACCAGGCACACTGTCCTGGTTTGAAACCAG 1140
AGGGGACAATAAAAAACCCTGATTCTGGTCTCTACTCACATAAAAGAAGCTTGTGAACA 1200
TTAAGTGGGAAGAGATTGCTACTAAATAACATACCTTGTAATTTCATCTTAATTAAAATA 1260
TACTTCTCTATATTATATATTTTA$_{(n)}$ 1284

Fig. 2

**Human IBR polypeptide**

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

Fig. 3A

**Mouse IBR polypeptide**

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAEKVIKGE EISVVPNRAL
DASLSPVILG VQGGSQCLSC GTEKGPILKL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTSPEADQP VRLTQIPEDP AWDAPITDFY
FQQCD

Fig. 3B

**Comparison of Human and Mouse IBR Polypeptide Sequences**

```
mIBR: 1   MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAEKVIKGEEISVVPNRALDASLSPVILG 60
          MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHA KVIKGEEISVVPNR-LDASLSPVILG IBRcon.
hIBR: 1   MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSPVILG 60

mIBR: 61  VQGGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120
          VQGGSQCLSCG--+-P+L-LEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF IBRcon.
hIBR: 61  VQGGSQCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWF 120

mIBR: 121 LCTSPEADQPVRLTQIPEDPAWDAPITDFYFQQCD 155
          LCT-PEADQPVRLTQ+PE+--W+APITDFYFQQCD IBRcon.
hIBR: 121 LCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD 155
```

Fig. 4

**Comparison of Human IBR and pro-IL-Ira Polypeptide Sequences**

```
hIL-lra:  38 FRIWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVP-------IEPHALFLGIHGGKM 90
             FR+ D   K  YL NNQL+AG L        V    E+I VVP        + P   + LG+ GG   con.
hIBR    :  9 FRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEEISVVPNRWLDASLSP--VILGVQGGSQ 66

hIL-lra:  91 CLSCVRSGDETKLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAM 150
             CLSC    G E   L LE VNI +L      K+ K F F R D G T+SFESAA PGWFLCT    con.
hIBR    : 67 CLSC-GVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVP 125

hIL-lra: 151 EADQPVSLTNMPDEG---VMVTKFYFQE 175
             EADQPV LT +P+ G      +T FYFQ+ con.
hIBR    : 126 EADQPVRLTQLPENGGWNAPITDFYFQQ 153
```

Fig. 5

**Recombinant IBR Polypeptides**

MVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

VLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

GSSVLSGALCFR MKDSALKVLY LHNNQLLAGG LHAGKVIKGE EISVVPNRWL
DASLSPVILG VQGGSQCLSC GVGQEPTLTL EPVNIMELYL GAKESKSFTF
YRRDMGLTSS FESAAYPGWF LCTVPEADQP VRLTQLPENG GWNAPITDFY
FQQCD

Fig. 6

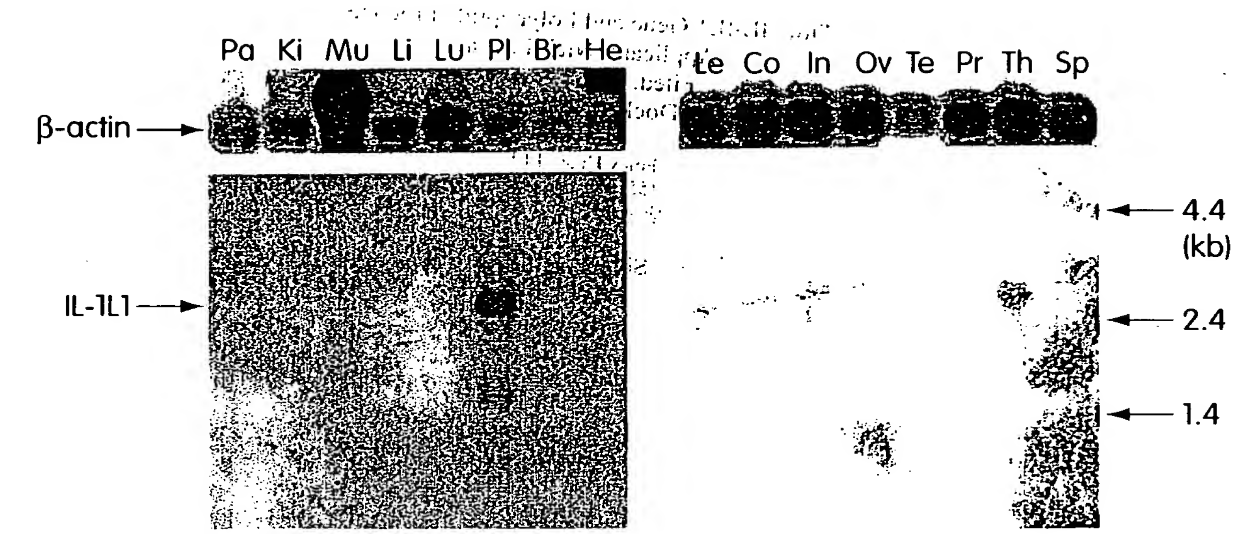
Pa
Ki
Mu
Li
Lu
Pl
Br
He
Le
Co
In
Ov
Te
Pr
Th
Sp
β-actin
IL-1L1
4.4 (kb)
2.4
1.4

Fig. 7A

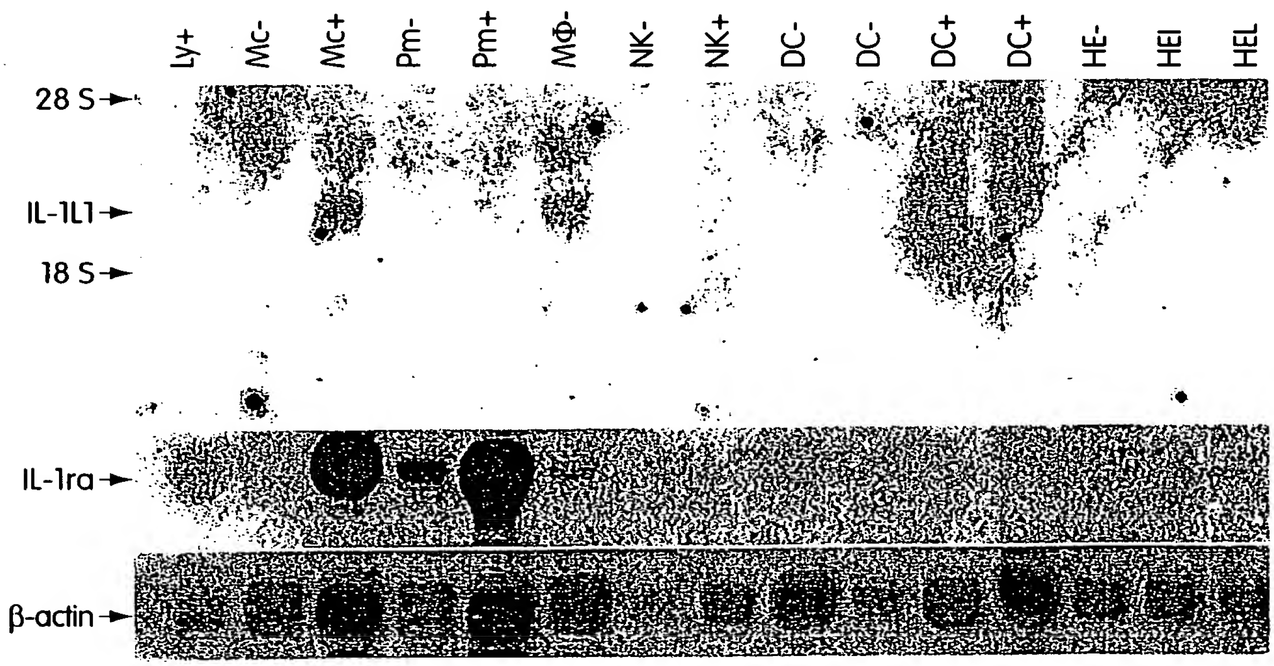
Ly+
Mc-
Mc+
Pm-
Pm+
MΦ-
NK-
NK+
DC-
DC-
DC+
DC+
HE-
HEI
HEL
28 S
IL-1L1
18 S
IL-1ra
β-actin

Fig. 7B

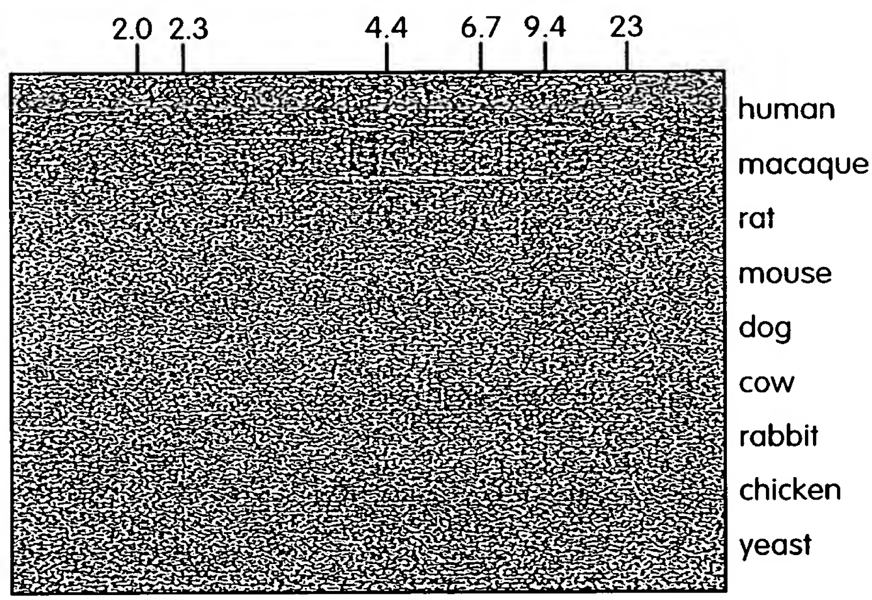
2.0
2.3
4.4
6.7
9.4
23
human
macaque
rat
mouse
dog
cow
rabbit
chicken
yeast

Fig. 8

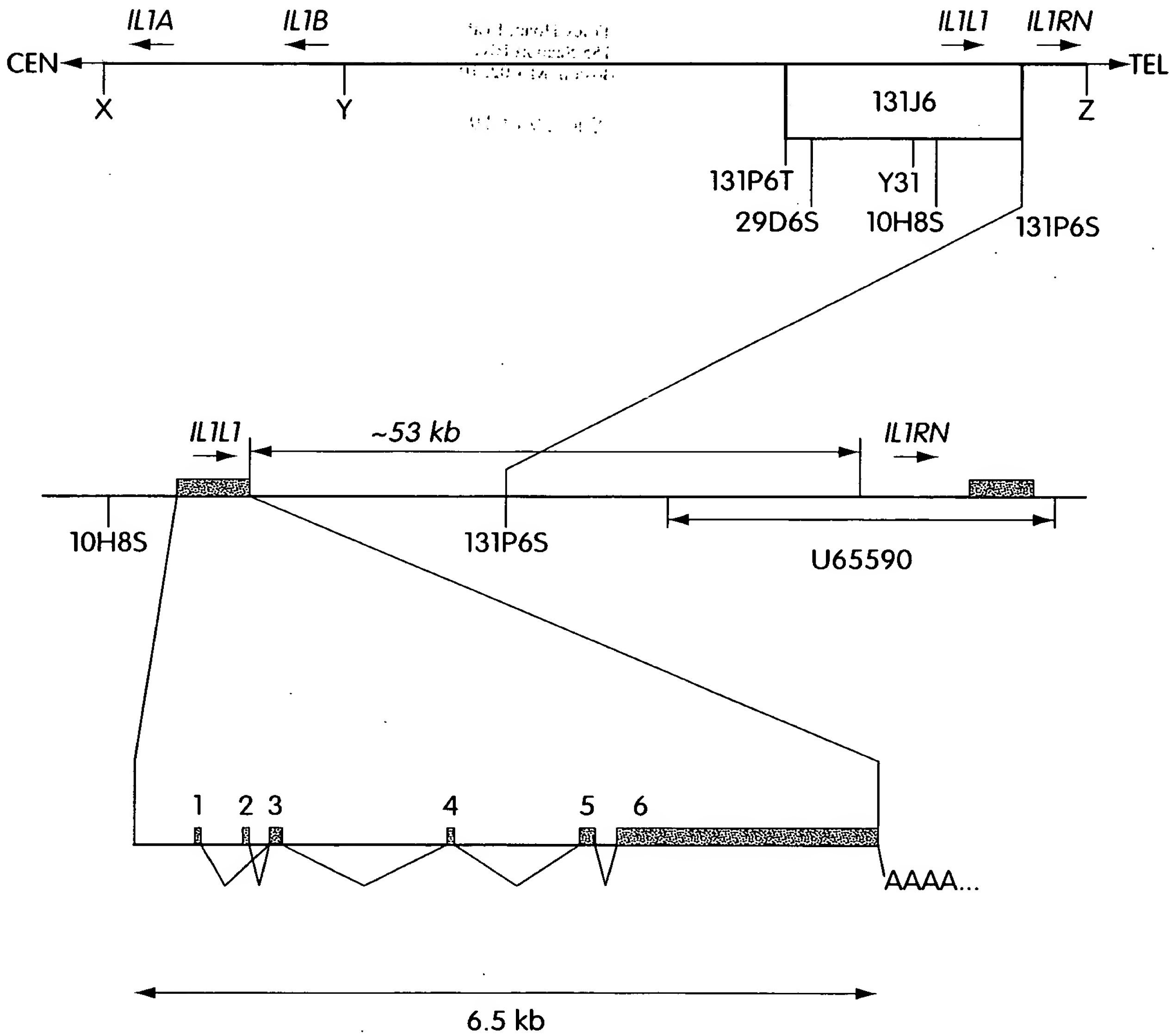
IL1A
IL1B
IL1L1
IL1RN
CEN
TEL
X
Y
Z
131J6
131P6T
29D6S
Y31
10H8S
131P6S
~53 kb
10H8S
131P6S
U65590
1
2
3
4
5
6
AAAA...
6.5 kb

Fig. 9

```
cDNA SEQUENCES CONTAINING EXON 1
CTGGCAATGGCAGGCAGGAAAGACAGAGGAAGGAAGGAGGGAGAAGGGAAGGAGTGAAGGAAGGAGTGAAAAA// exon 3
^                                ^
-74'   M  A  G  R  K  D  R  G  R  K  E  G  E  G  K  E ***          ***

cDNA SEQUENCES CONTAINING EXON 2
TTGGAGGAACAGGCAGACTCCACAGCTCCCGCCAGGAGAAAGGAACATTCTGAG// exon 3
^                                  ^                ^     ^
-54                                                 ^
```

Fig. 10A

| 5' flank | start | exon | start seq | cDNA | end seq | end | 3'flank |
|---|---|---|---|---|---|---|---|
| | + 451 | 1 | CTGGCAATGG | -74'- -1' | AGTGAAAAAG | + 524 | gtaaggaaga |
| | + 969 | 2 | TTGGAGGAAC | -54 - -1 | ACATTCTGAG | +1022 | gtatgctctg |
| tccaaaatag | +1193 | 3 | GGGAGTCTAC | 1 - 56 | TGTGCTTCCG | +1248 | gtgagtgtat |
| gatgtttcag | +2631 | 4 | AATGAAGGAC | 57 - 142 | GTCATTAAAG | +2716 | gttggtgatg |
| tttcccacag | +3905 | 5 | GTGAAGAGAT | 143 - 270 | AACACTAGAG | +4032 | gtgagacttg |
| ctgccggcag | +4234 | 6 | CCAGTGAACA | 271 - 2559 | AGAGAAAGAG | +6522 | aaacaaatgc |

Fig. 10B

```
IL-1L1   MVLSGALCFR(2)MKDSALKVLYLHNNQLLAGGLHAGKVIKG(1)EEISVVPNRWLDASLSP
IL-1ra ..RKSSKMQAFR(2)IWDVNQKTFYLRNNQLVAGYLQGPNVNLEE(1)KIDVVP-----IEPHA

IL-1L1   VILGVQGGSQCLSCG-VGQEPTLTLE(3)VNIMELYLGAKESKSFTFYRRDM..
IL-1ra   LFLGIHGGKMCLSCVKSGDETRLQLE(3)VNITDLSENRKQDKRFAFIRSDS..
```

Fig. 10C

1 CATGAGCAAA GATGTTAATA CAAAGATGTT TGTCACAACA TGGTTTTCAA TAGCAAAAAA

61 AGAGAGAAAA ATATATAAAA GACAAATAAC AGTGGATAGG TTTCAATAAA TAATGTTACA

121 GTGATACAGT TAAATACTAT ACAGCTATTG AAGCATGTCA TTATTCATAT TTAGTATGGA

181 AAGATATTTT GCTATTTTGC TACATGAAAA AATGAGGTTG GAAAAAGTAT AGGTTTTGTG

241 AATCTGTTGT ATGAAAGCTG TCTATAGTTA CATGTGTATG TGTGTGGAGG AAAAAGTGTT

301 GTCATTGGTT TTCTGATGAT GCACTCAGAA AAGACAAGTA TTCACATTTT TTCTTGTGGC

361 TGATCTGGAT TTTCAGGTTT TTCTACAATG AACATGTAGG CTGAACATTC CCTAAGCAGG

421 AGAGTCCCAC CTCTAACATC TCCTGTAGGC CTGGCAATGG CAGGCAGGAA AGACAGAGGA

481 AGGAAGGAGG GAGAAGGGAA GGAGTGAAGG AAGGAGTGAA AAAGGTAAGG AAGAAAGGGA

541 ATAGGGGAGG AAGGGAGGAA ATGGGAAGGG AAAGAAGGAA AGGAAGGAAA GAGGGAGGGA

601 AGAAAGGAAG GGAAAAGGGA GGGAGTGAGT GAATGAAAGA TGGAAAGAAG GAAGAAAGGG

661 AGGGAGGCAG GGAGGAAAGA AAGTTGCGCT TCCCTTGAGC TGCCATGGGC ACTGACTCTT

721 AGGGTCTGAA AGCCCCTGAG ATGCAAAAGC CTAGTGCTCA CAAAGAGCTG GAAAGCCTCA

781 AGGAAGTTCT TCAATATTTC TGGAAGGAAA CTGTCTCCAG AAGCTTCCCT CCCCACGACA

841 GATAATGAGC AGCAAGTGCT TCTGGCGACT TAGGGTGATG TGAAATCACG CTGGGAATCC

901 TGCTCCTCCT CAGGTCCTGG CAGTTTCAGG GCCCCTCCCT AGGCCTTACT TAAAAGGCTG

961 AGGCATCCTT GGAGGAACAG GCAGACTCCA CAGCTCCCGC CAGGAGAAAG GAACATTCTG

1021 AGGTATGCTC TGGGGCGCTG GTGGTACCGG AGCTCTCTCC TGACCCCAGA CCCAGAATCT

Fig. 11

1081 GCTCCGTGGA GGCTGTTCAC ATGCTGGGGA GCTCGGTGCA GCTGCTTGCT CCCCAGACCC

1141 CAGCCAACTC AGCCTCTCTC TCCATGATTT TCTGTTGTTT ATTCCAAAAT AGGGGAGTCT

1201 ACACCCTGTG GAGCTCAAGA TGGTCCTGAG TGGGGCGCTG TGCTTCCGGT GAGTGTATGA

1261 GGCCCTGGTT TGGTGGTGTC CTCCGGAGGA AGTGAGTTCT GGATAGACCC GTTGTCCAGC

1321 TCTGAGCAGG AGGGAGGAAG GGAGGGGCTG CCATTGCAGC TGGGAAATTG TGACCAGCAC

1381 CTCATTGCTC TTAGAGTTTT CCCAGCCTTT TTCAAATAGG GGCAGGACTG GGGCAGGCCA

1441 TCTCACAAGG GGTCCCTGAT GCTGAGGGGG ACAAGTGAAC CTCCCAGTCT AGAGCTCCAG

1501 CCAAGTCTAT CCAAGGTGGG AACGGGGGCC AGGATCCCTG CTCAGAGCTC CGCCATTGTC

1561 CCCCATCACA GTGAATGGAT GTAAGCTCAC CCACTCTGTG CCCCTACCTC CCTGCTACTC

1621 TTTGGGGATA ATAATAAAAC AAAAACCATT ACCATCAGCC AGTCTGTCCA CCCACTGGCA

1681 TGTACCAAGC CAGACACTCT GCCGTGTTCT GGGCTTAACA ACAGAGGATG AGAGTGGTCC

1741 TTTCTCTCAG TCTAATAAAG CACTTCCCAC GATGTGTTCT ATGGGACTCG ATTAGAGGAG

1801 TCCCACAGAG GCATCCAGGA GATGCTTTAC ACAGTGGAGC TCTCTGATCA AGTAAATGCA

1861 GGGAATTCTG CTTTCTACAT CCTCTCATAA GAGAACCACA GCCCAGCTCA GCATATGAGT

1921 GACTGAGGTT TTCTGAAGTA AGGCAACTTG TTGAATCGTA TTTAGCTATG CATCGACCCA

1981 ATTTTTACAC TGCATCCTTT TCCCCCATAT AACTTTTGGA GAAACCCACT TTAGGATACA

2041 TCTTCCACCT CATAGGATGC CAGGAAATCA ACTGAGTTCA AAGATGAGAA ACAACTTTGA

2101 AAAGTTAAAT AAAAGAAATT TAAATTTAAA GAAACTCCTC ACTTAGTAAG GAATATATGA

2161 CCAAATAGAA ATACATGTAT CTTGAAGAAT TGAAGAATCA GGCTTTAACG TGGAAGAGGC

Fig. 11 (Continued)

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2221 CTGGATGTTA TCCAACCCAT CATCTTAGTG TAGCAATGGG GAGGCTCAGG CCCAGAGTGG

2281 GCGAGAGAGT TGTCTCCTGC GACTCAGCAG CATTGGAGGC ATAGATGGGG CAAGAACCTA

2341 GGGCTCTGAC TCACCGTGCA GCTTCTCTTC CAACAGGAGA TGGGTTGGGG CAGAAAAGGT

2401 TGAATAGGGT GAAGGAGCAA ACCACAGACT CCAGTGGGAG ACTGTGGGGT CATCCTCCTT

2461 GTAGGGCATG AGCCCAGCAG GGCTGGGAGA CAAGGCTGTG CTGTTACTTC TGGCACAGTA

2521 GGAAGAAAGA GAGACAAAAT GCCTGAGATC AGGGGGTTCT CTGGATCCAG GGCATGCTGG

2581 AGTGTCCACC CTCCTCCTAA TGTAGTCCTC ACCCCTTCCT GATGTTTCAG AATGAAGGAC

2641 TCGGCATTGA AGGTGCTTTA TCTGCATAAT AACCAGCTTC TAGCTGGAGG GCTGCATGCA

2701 GGGAAGGTCA TTAAAGGTTG GTGATGAAAC ATGACCCACT TTCCTTGGTC TCTATACACT

2761 CTCAGGGGAG GGGGCCTGAA GAGGGCTTAG AATAGTCATA CAGATTAGCA TAGGCCTACA

2821 GAGCCCAGGC ATTAGGGCAG CACAAACCAG GCTCTAAGCA AAGGCAAATA AAATACTACA

2881 CCTCTCAGCA AAGTGAAGAC ACACGCTCTG GGGCCACCTG AAGCTTCTGT GCAGAAGTGA

2941 GAATGTTTTC CAAGAGGCTT GTCTTGTCAT TCCCTTACAG GTAGATTTAG GTCAAGCATT

3001 GCATTCCCTG GGAGCCAGTA AGTACCAAGG AGAGAACTAA CGTAGATTCT CTATACCTTT

3061 TTTCCCATAT GGGAGTGGGT TTCTGCCTCT CCACCCTGGG TCCCCTCTGC TCTCTGAAGA

3121 TCCTCAGTCA CTTAGAGTGG AGGGACCCAG AGAACAGGTG GCATTGTTGG ACCTCCTGCT

3181 TGCTCACTCT GCCCCATGCA CTGCAACAGG TCCCTCTCTA AAATAGTTTG CACCTGCCCA

3241 CCTGGGGCAC CCTTGCTGAG CACAGATGCC AGGTAGATCC TTCAGCTAGG CCATATGTGT

3301 ATGTGTGTGC TTACTGGTGT ATGTATGTGT GCATGCAGGC ATATATGTGT GAGCATATGT

Fig. 11 (Continued)

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3361 GTGCATGCAT GTATCTGTAT GTAACCATGT ATGTGTGAGT GCAGGTATGT AGGTATGAGC
3421 ATGTGTGTGT ATATGTATAT GTGTGCATGC ATGTATCTGT GCATGTATGT ATCTGATGTA
3481 TGTGGGTGGT GAGGGGATGT ACAGAGAGGA ATGAGACCCT CTTTTGCTCT CAGCAACCTC
3541 ACAGGGTGTA GAAAGTTGTC CAAACAATTC CAAAGGGGGG CTTATTAAGA CAGGGTTCAG
3601 AAAAAGGCCT GAGACCCAAG GGGCATTAAA GGAGGGGGTT GAGTCTATTT TGGGTTGTAG
3661 AGGCTTGAAG ATTTGACCCT GAACTAGAGG GTGGAGTGGA GGTGGTACAA TGTGCTTCCA
3721 TGCCTTGATG TCCACTCTGG GCCAGTGGAC AGGAGAAGCC ATGTCATGAC AGCTGCTGAG
3781 AAGCCTCCCT TCTGCCCAGC CTGGGGGCAG GCCGTCTCAC AGCAGTCCTG TGCCCTAGAG
3841 CCCAGGACAG GGGAAGAAGG AGGGAAAGGC ATCCAGGGCC CTGCATCTGG CCTCTTTCCC
3901 ACAGGTGAAG AGATCAGCGT GGTCCCCAAT CGGTGGCTGG ATGCCAGCCT GTCCCCCGTC
3961 ATCCTGGGTG TCCAGGGTGG AAGCCAGTGC CTGTCATGTG GGGTGGGGCA GGAGCCGACT
4021 CTAACACTAG AGGTGAGACT TGGGGCATCC TCACTGGGGA CTCAGCCACA GATGCTGAGC
4081 CTACTGAAGC CGGGCAGCCC ACAGCCCTGG TGCTGTGGGA CACCCTAGCA GGATTCTGTT
4141 GATGGCAGCT TTGCCTCCTC CCTAAGGATC CTGCCCAGCC CTCCCTCTGC CCCTGCTTCT
4201 GCCCTCACCT GACCTCCCCT CCTCTGCCGG CAGCCAGTGA ACATCATGGA GCTCTATCTT
4261 GGTGCCAAGG AATCCAAGAG CTTCACCTTC TACCGGCGGG ACATGGGGCT CACCTCCAGC
4321 TTCGAGTCGG CTGCCTACCC GGGCTGGTTC CTGTGCACGG TGCCTGAAGC CGATCAGCCT
4381 GTCAGACTCA CCCAGCTTCC CGAGAATGGT GGCTGGAATG CCCCCATCAC AGACTTCTAC
4441 TTCCAGCAGT GTGACTAGGG CAACGTGCCC CCCAGAACTC CCTGGGCAGA GCCAGCTCGG

Fig. 11 (Continued)

4501 GTGAGGGGTG AGTGGAGGAG ACCCATGGCG GACAATCACT CTCTCTGCTC TCAGGACCCC

4561 CACGTCTGAC TTAGTGGGCA CCTGACCACT TTGTCTTCTG GTTCCCAGTT TGGATAAATT

4621 CTGAGATTTG GAGCTCAGTC CACGGTCCTC CCCCACTGGA TGGTGCTACT GCTGTGGAAC

4681 CTTGTAAAAA CCATGTGGGG TAAACTGGGA ATAACATGAA AAGATTTCTG TGGGGGTGGG

4741 GTGGGGGAGT GGTGGGAATC ATTCCTGCTT AATGGTAACT GACAAGTGTT ACCCTGAGCC

4801 CCGCAGGCCA ACCCATCCCC AGTTGAGCCT TATAGGGTCA GTAGCTCTCC ACATGAAGTC

4861 CTGTCACTCA CCACTGTGCA GGAGAGGGAG GTGGTCATAG AGTCAGGGAT CTATGGCCCT

4921 TGGCCCAGCC CCACCCCCTT CCCTTTAATC CTGCCACTGT CATATGCTAC CTTTCCTATC

4981 TCTTCCCTCA TCATCTTGTT GTGGGCATGA GGAGGTGGTG ATGTCAGAAG AAATGGCTCG

5041 AGCTCAGAAG ATAAAAGATA AGTAGGGTAT GCTGATCCTC TTTTAAAAAC CCAAGATACA

5101 ATCAAAATCC CAGATGCTGG TCTCTATTCC CATGAAAAAG TGCTCATGAC ATATTGAGAA

5161 GACCTACTTA CAAAGTGGCA TATATTGCAA TTTATTTTAA TTAAAAGATA CCTATTTATA

5221 TATTTCTTTA TAGAAAAAAG TCTGGAAGAG TTTACTTCAA TTGTAGCAAT GTCAGGGTGG

5281 TGGCAGTATA GGTGATTTTT CTTTTAATTC TGTTAATTTA TCTGTATTTC CTAATTTTTC

5341 TACAATGAAG ATGAATTCCT TGTATAAAAA TAAGAAAAGA AATTAATCTT GAGGTAAGCA

5401 GAGCAGACAT CATCTCTGAT TGTCCTCAGC CTCCACTTCC CCAGAGTAAA TTCAAATTGA

5461 ATCGAGCTCT GCTGCTCTGG TTGGTTGTAG TAGTGATCAG GAAACAGATC TCAGCAAAGC

5521 CACTGAGGAG GAGGCTGTGA TGAGTTTGTG TGGCTGGAAT CTCTGGGTAA GGAACTTAAA

5581 GAACAAAAAT CATCTGGTAA TTCTTTCCTA GAAGGATCAC AGCCCCTGGG ATTCCAAGGC

Fig. 11 (Continued)

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5641 ATTGGATCCA GTCTCTAAGA AGGCTGCTGT ACTGGTTGAA TTGTGTCCCC CTCAAATTCA

5701 CATCCTTCTT GGAATCTCAG TCTGTGAGTT TATTTGGAGA TAAGGTCTCT GCAGATGTAG

5761 TTAGTTAAGA CAAGGTCATG CTGGATGAAG GTAGACCTAA ATTCAATATG ACTGGTTTCC

5821 TTGTATGAAA AGGAGAGGAC ACAGAGACAG AGGAGACGCG GGGAAGACTA TGTAAAGATG

5881 AAGGCAGAGA TCGGAGTTTT GCAGCCACAA GCTAAGAAAC ACCAAGGATT GTGGCAACCA

5941 TCAGAAGCTT GGAAGAGGCA AAGAAGAATT CTTCCCTAGA GGCTTTAGAG GGATAACGGC

6001 TCTGCTGAAA CCTTAATCTC AGACTTCCAG CCTCCTGAAC GAAGAAAGAA TAAATTTCGG

6061 CTGTTTTAAG CCACCAAGGA TAATTGGTTA TGGCAGCTCT AGGAAACTAA TACAGCTGCT

6121 AAAATGATCC CTGTCTCCTC GTGTTTACAT TCTGTGTGTG TCCCCTCCCA CAATGTACCA

6181 AAGTTGTCTT TGTGACCAAT AGAATATGGC AGAAGTGATG GCATGCCACT TCCAAGATTA

6241 GGTTATAAAA GACACTGCAG CTTCTACTTG AGCCCTCTCT CTCTGCCACC CACCGCCCCC

6301 AATCTATCTT GGCTCACTCG CTCTGGGGGA AGCTAGCTTC CATGCTATGA GCAGGCCTAT

6361 AAAGAGACTT ATGTGGTAAA AAATGAAGTC TCCTGCCCAC AGCCACATTA GTGAACCTAG

6421 AAGCAGAGAC TCTGTGAGAT AATCAATGTT TGTTGTTTTA AGTTGCTCAG TTTTGGTCTA

6481 ACTTGTTATG CAGCAATAGA TAAATAATAT GCAGAGAAAG AGAAACAAAT GCATTTGTTT

Fig. 11 (Continued)

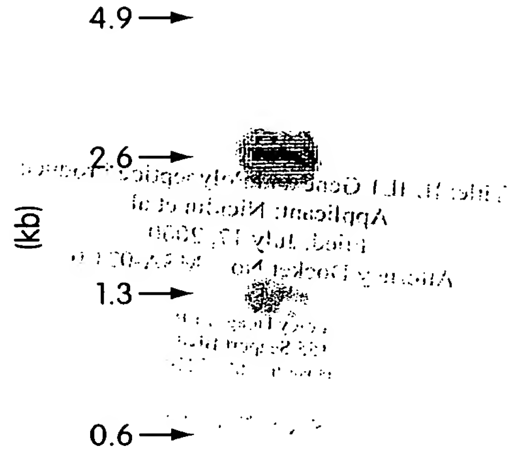


Fig. 12A

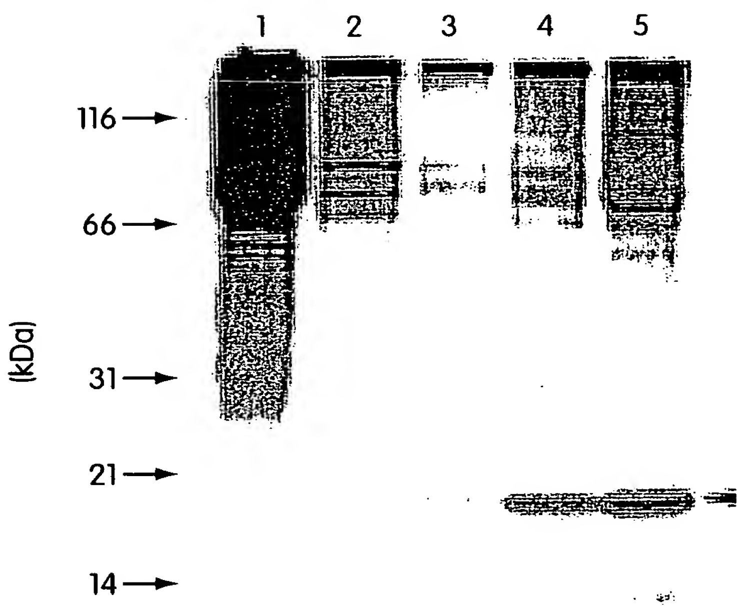


Fig. 12B

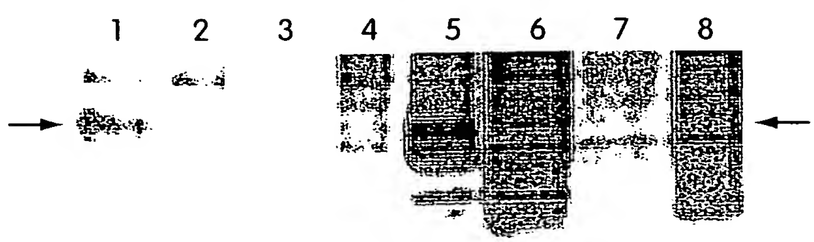


Fig. 12C

```
                           Sheet 1  Sheet 2  Sheet3           Sheet 4
                        *  ** ** **     **     ***    *     * *    **
                           >>>>>>>>  >>>>>    >>>>>           >>>>>>>
hIL-1L1                 MVLSGALCFRMKDSALKVLYLH NNQLLAG GLHAGKVIKGEEISVVP 46
mIL-1L1                 MVLSGALCFRMKDSALKVLYLH NNQLLAG GLHAFKVIKGEEISVVP 46
hIL-1ra             RPSGRKSSKMQAFRIWDVNQKTFYLR NNQLVAG YLQGPNVNLEEKIDVVP 50
hIL-1beta                APVRSLNCTLRDSQQKSLVMSGPYELKAL HLQGQDMEQQVVFSMSF 46
hIL-1alpha SAPFSFLSNVKYNFMRIIKYEFILNDALNQSIIRANDQYLTAAALHNLDEAV KFDMGAY 59
hIL-18            YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAP RTIFIISMY 52

                   Sheet 5   Sheet 6     Sheet 7               Sheet 8
              *   * ******   * *  * * ** *********                **
                    >>>>>     >>>>>> >  >>>>>>>>                >>>>>
hIL-1L1    NRWLDASLSPVILGVQG GSQCLSCG VGQEPTLTLEPVNIMELYLGAKESKSFTFYRR 103
mIL-1L1    NRALDASLSPVILGVQG GSQCLSCG TEKGPILKLEPVNIMELYLGAKESKSFTFYRR 103
hIL-1ra         IEPHALFLGIHG GKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRS 103
hIL-1beta  VQGEESNDKIPVALGLK EKNLYLSCVLKDDKPTLQLESVDPKNYPK KKMEKRFVFNKI 104
hIL-1alpha KSSKDDAKITVILRIS KTQLYVTAQ DEDQPVLLKEMPEIPKTIT GSETNLLFFWE 114
hIL-18     KDSQ PRGMAVTISVKCEKISTLSCE  NKIISFKEMNPPDNIKDTKSDIIFFQRSVP 107

                Sheet 9     Sheet 10   Sheet 11        Sheet 12
            *  * * *   * * *  ***    *  ******      * *** **
           >>> >>>>>>>   >>>>>>     >>>>>>>          >>>>>>
hIL-1L1    DMGLTSSFESAAYPGWFLCTVPEADQPVRLTQLPENGGWNAPITDFYFQQCD   155
mIL-1L1    DMGLTSSFESAAYPGWFLCTSPEADQPVRLTQIPEDPAWDAPITDFYFQQCD   155
hIL-1ra    DSGPTTSFESAACPGWFLCTAMEADQPVSLTNMPDEG   VMVTKFYFQEDE   152
hIL-1beta  EINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQ    DITDFTMQFVSS  153
hIL-1alpha THGTKNYFTSVAHPNLFIAT KQDYWVCLAGGP P     SITDFQILENQA   159
hIL-18     GHDNKMQFESSSYEGYFLACEKERDLFKLILKKEDELG DRSIMFTVQNED   157
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Fig. 13